Structure, function and evolution of the microbiota thriving at the root-soil interface

Bulgarelli, Davide

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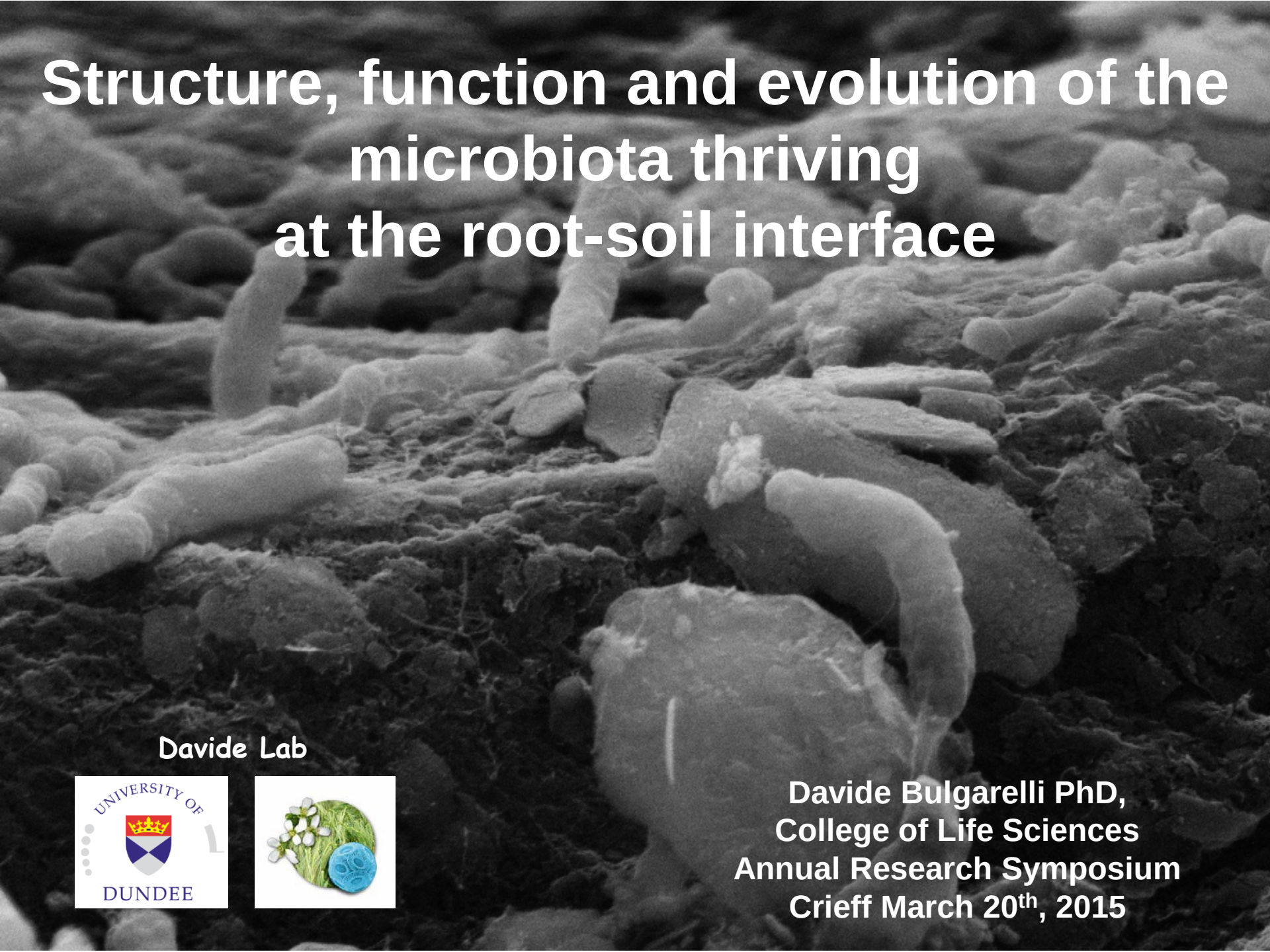


Davide Lab

Davide Bulgarelli PhD,
College of Life Sciences
Annual Research Symposium
Crieff March 20th, 2015

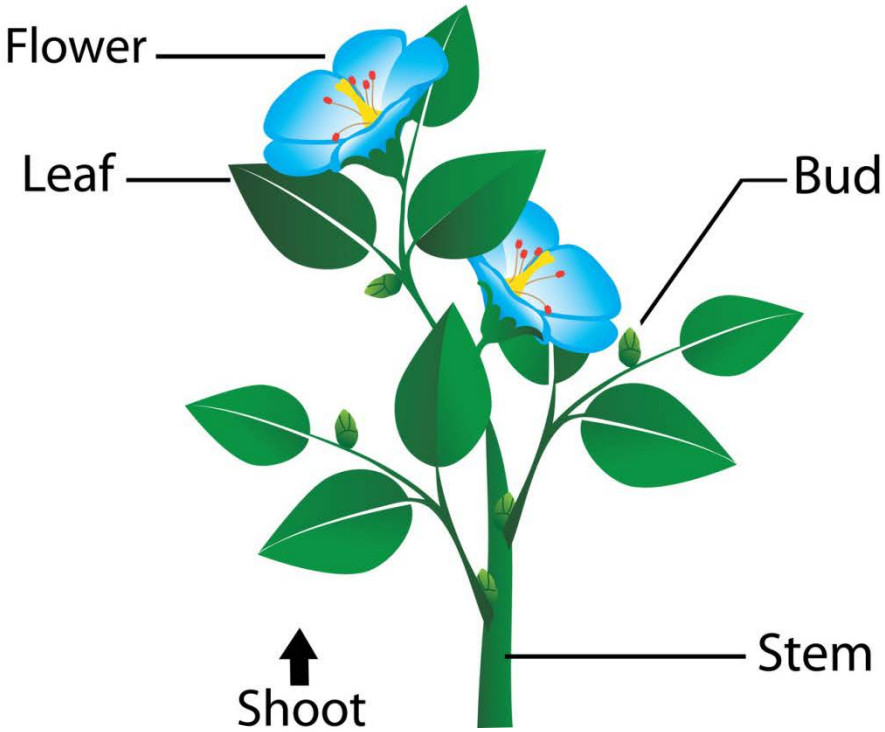
The menu

The root-soil interface

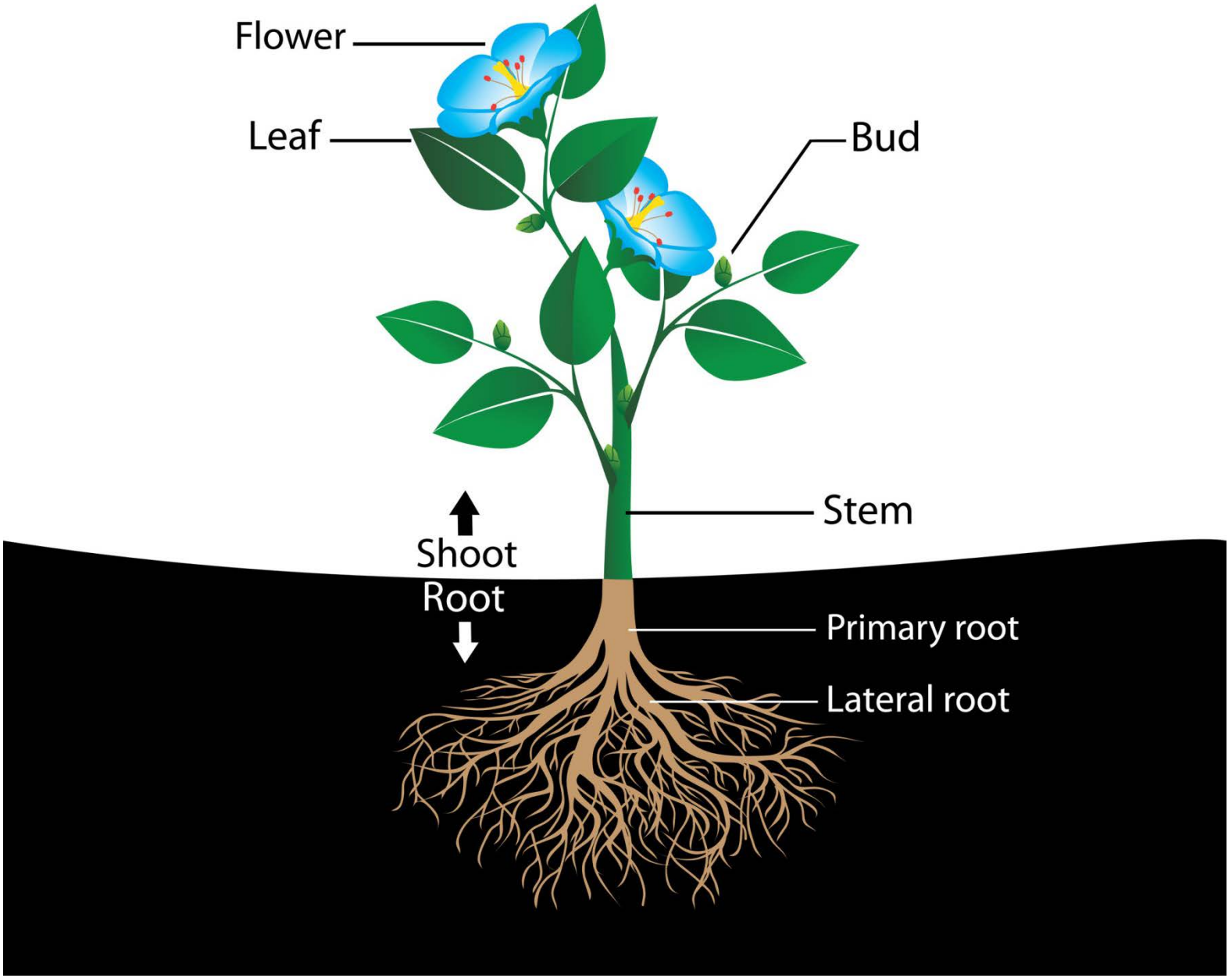
The barley microbiota

What’s next?

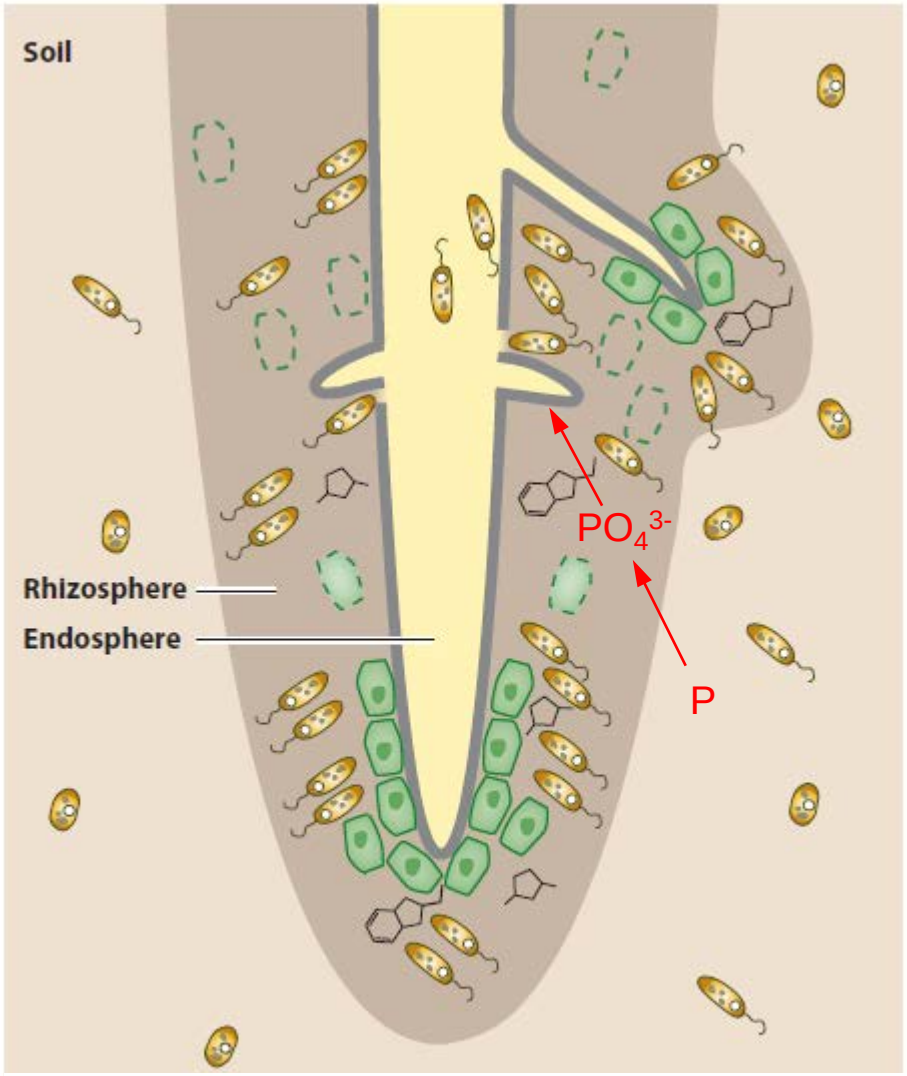
Spring is coming…

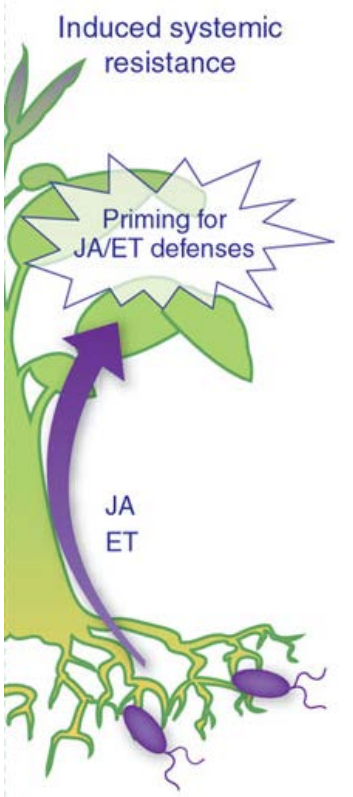


This is a plant!



“Plants wear their guts on the outside”

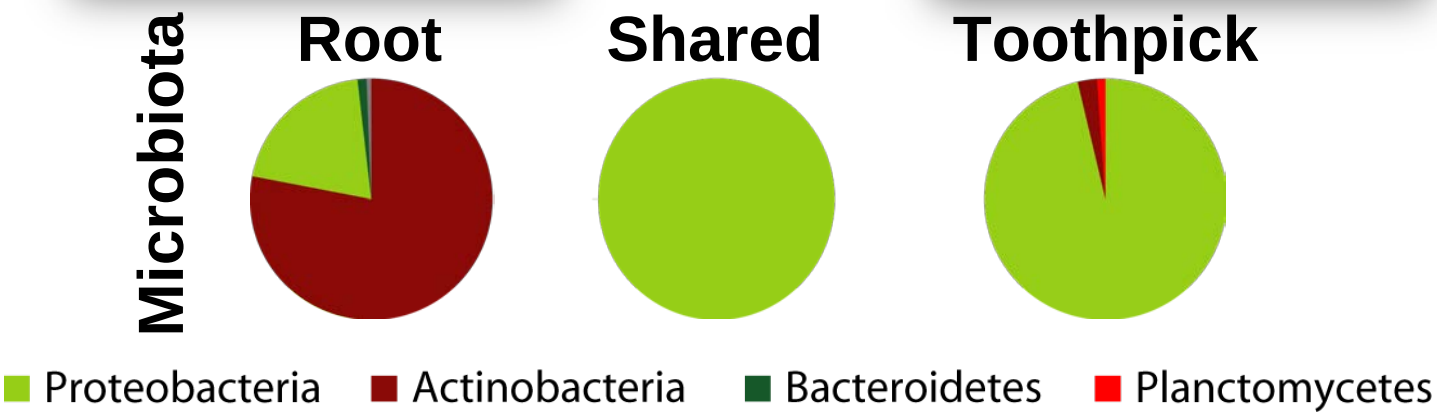




Plant Microbiota

Structure? Functions? Host Control?

Are plants and toothpicks different?



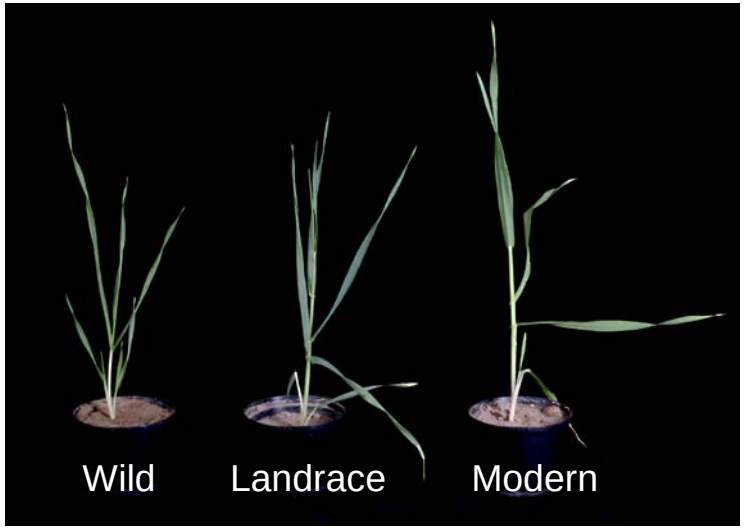
Bulgarelli *et al*. (2012) , Nature 488:91

Barley as a model to study crop-microbiota interactions

- Staple Crop: world 4th most cultivated
- Interfertility with wild progenitors
- Diploid genome
- Large germplasm collections: accessions & mutants
- -omics resources
- *Gene-ome* available

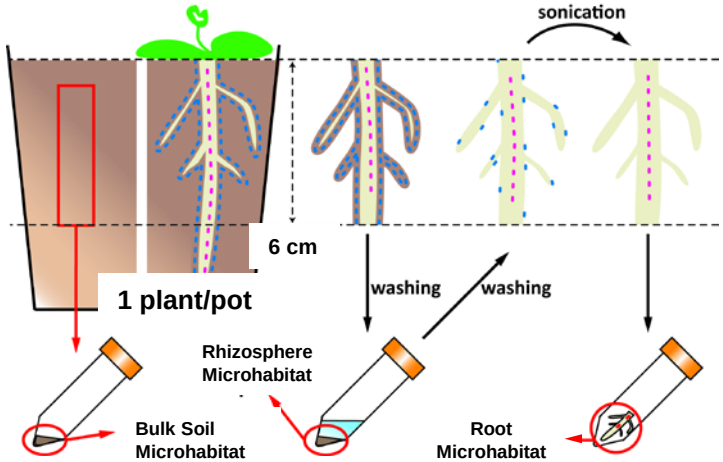
Do crop plants and their wild relatives recruit different microbiota?

I) Plants grown in natural soil

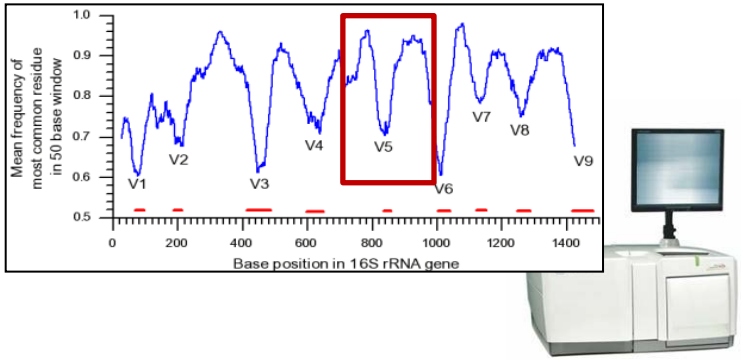


Golm soil, 2 seasonal samplings

II) Sample fractionation & DNA isolation



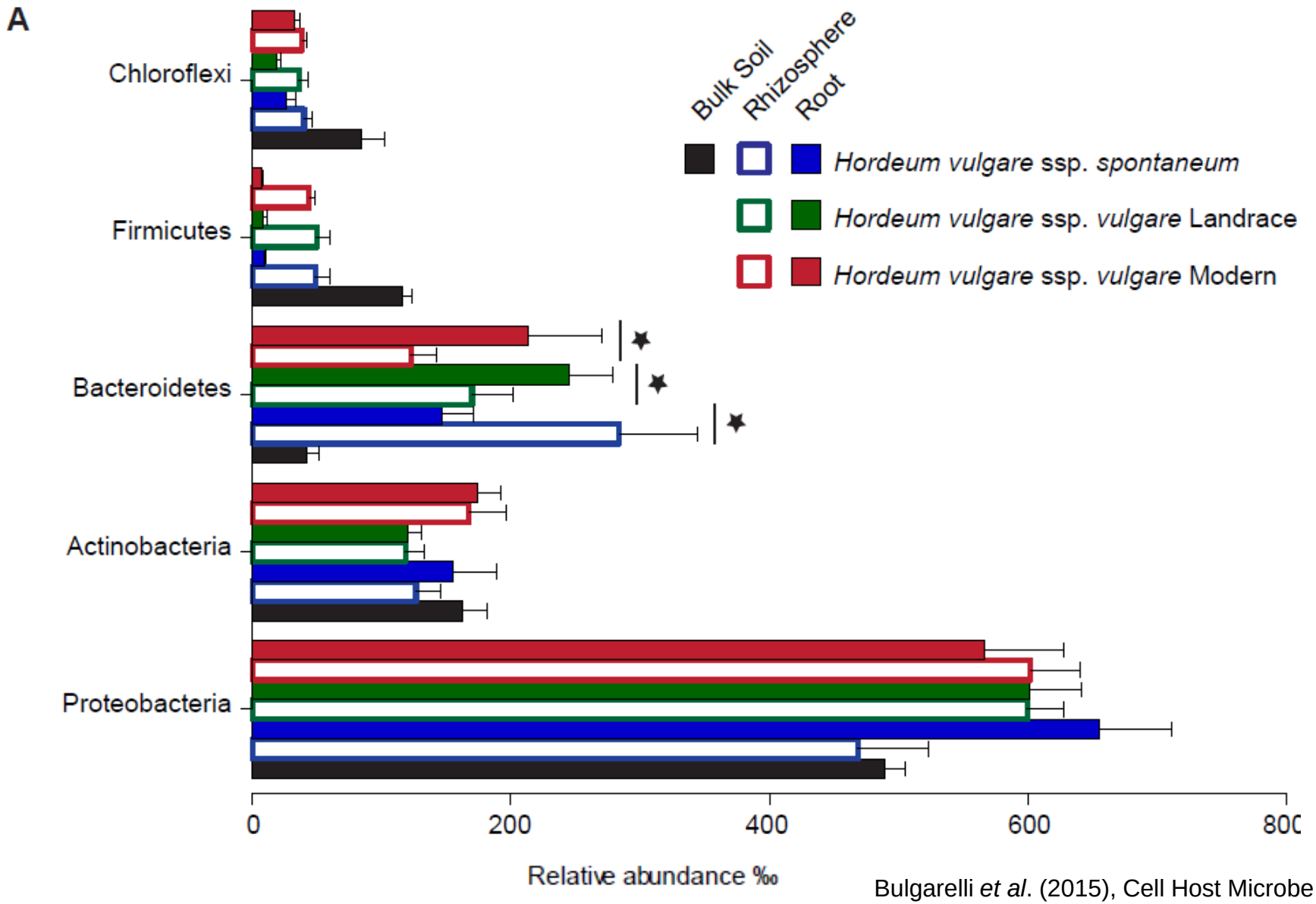
III) Pyrosequencing of the 16S rRNA gene



IV) Sequence analysis

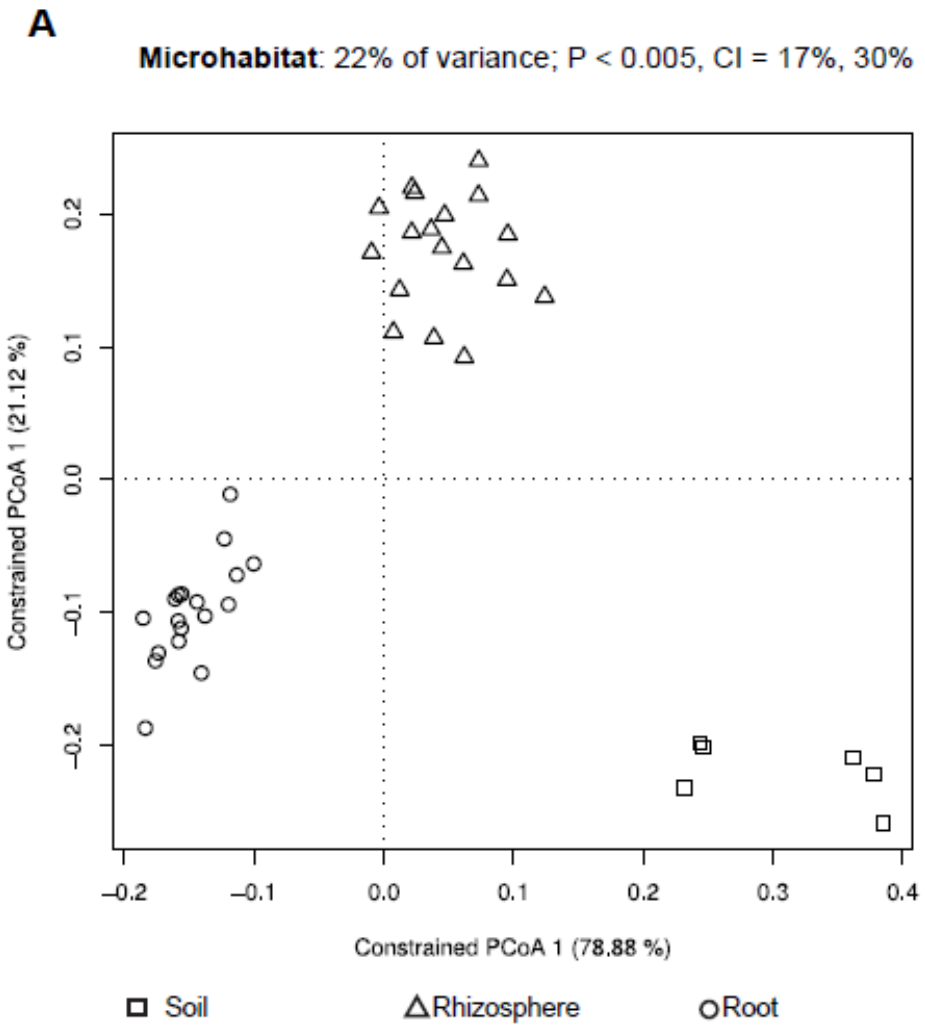
- Operational taxonomic units (**OTUs**) definition
- Taxonomic information
- Structural analysis using ecological indices and multivariate statistics

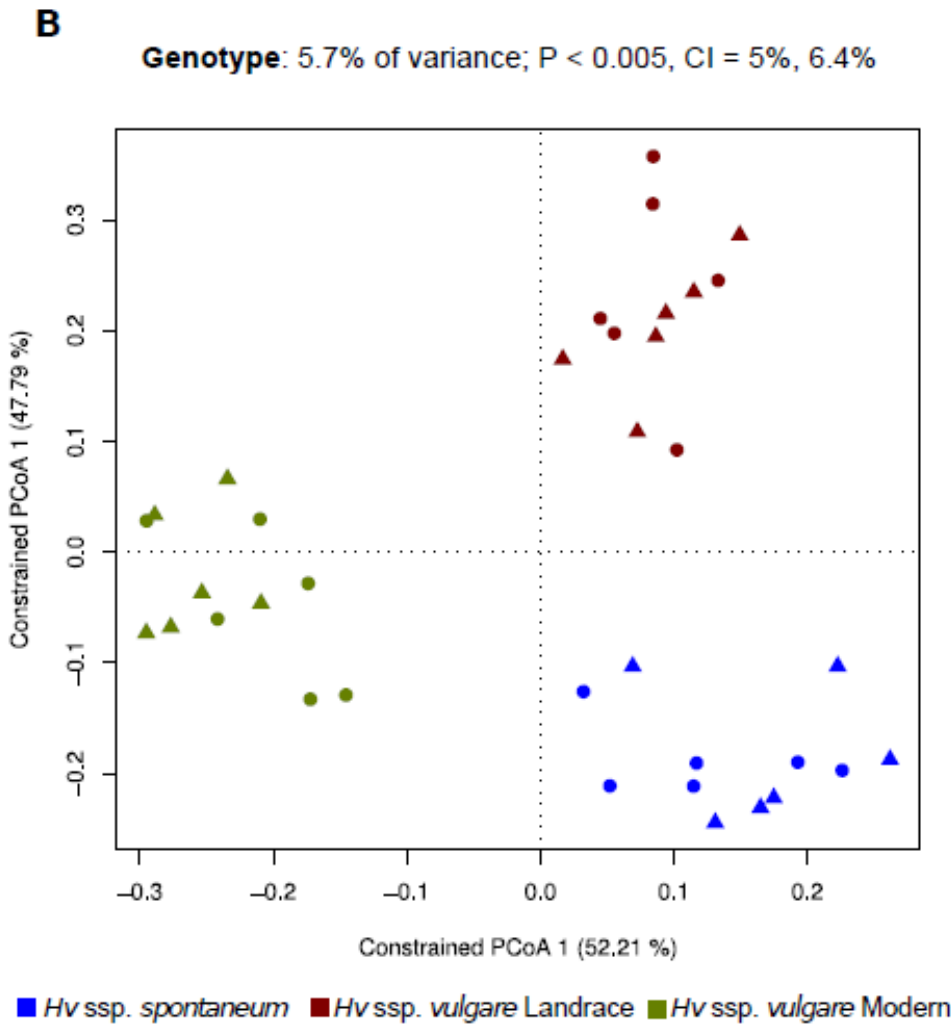
The barley bacterial microbiota is a gated community



Bulgarelli *et al*. (2015), Cell Host Microbe 17:1

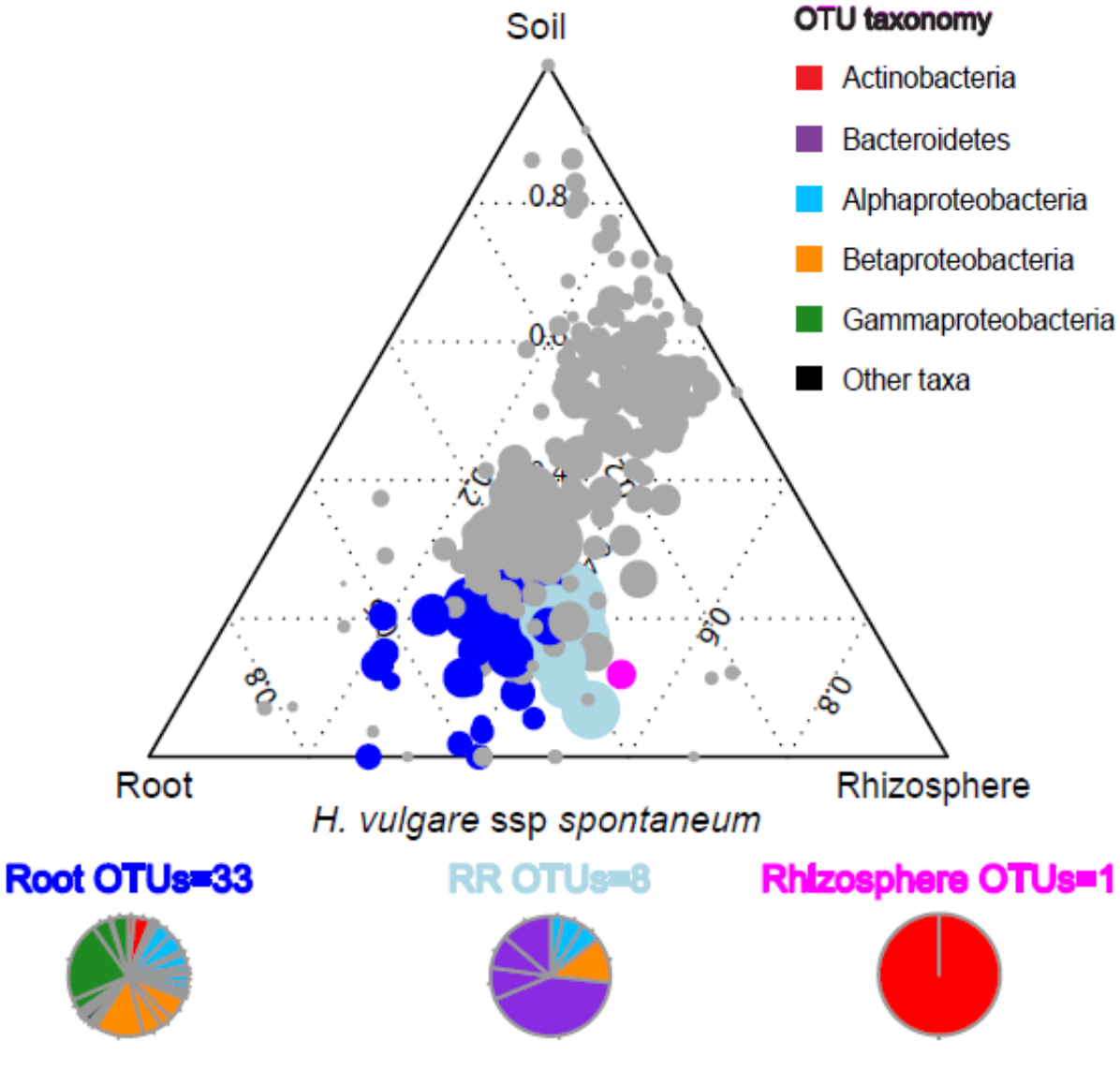
The habitat determines the structure of the microbiota…
…and the host genotype fine tunes its composition

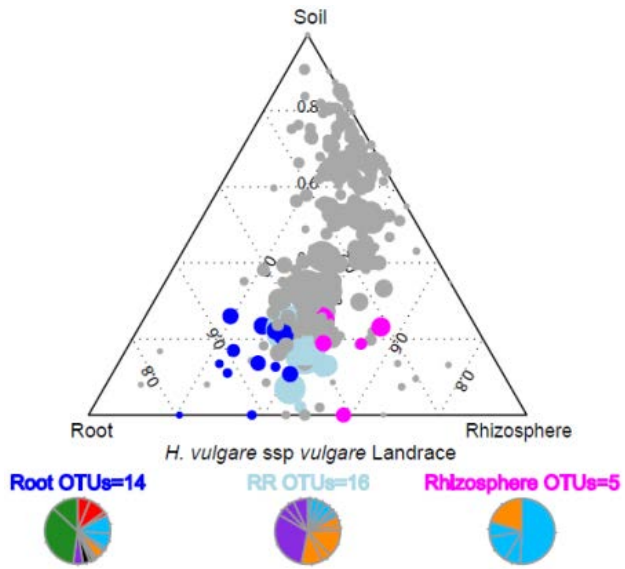


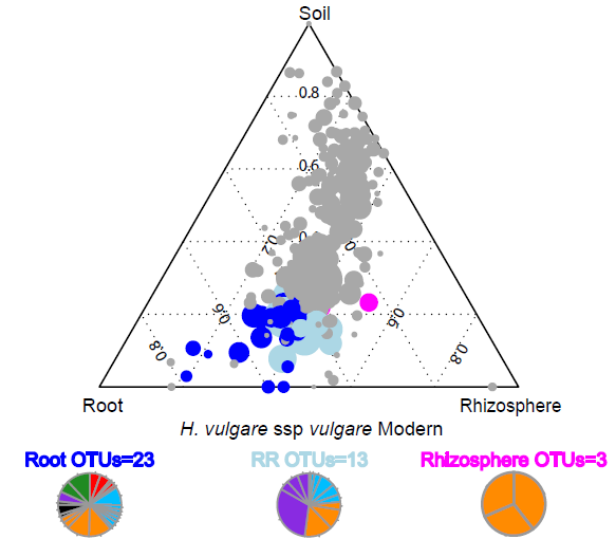


Bulgarelli *et al*. (2015), Cell Host Microbe 17:1

Barley shapes the root and rhizosphere microbiota

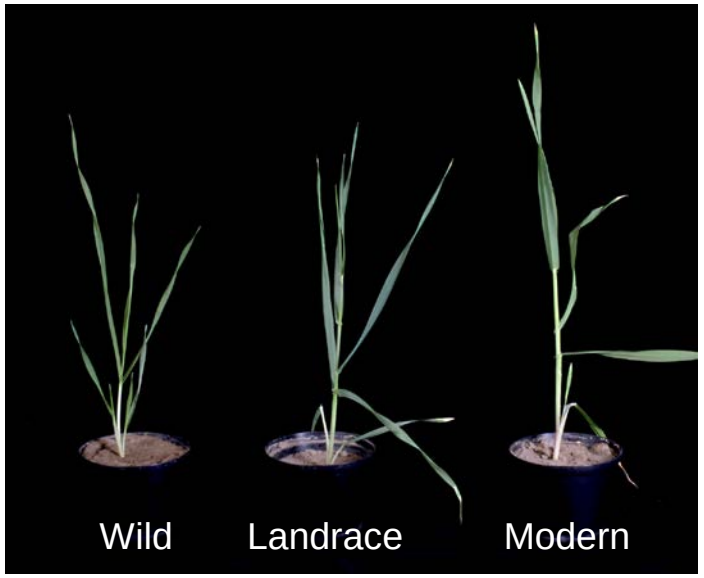






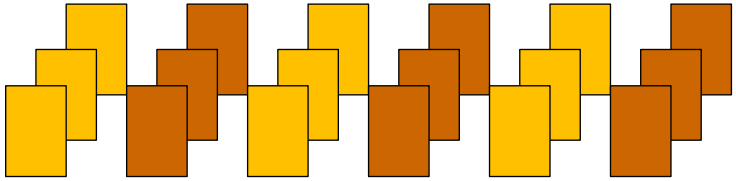
Bulgarelli *et al*. (2015), Cell Host Microbe 17:1

Shotgun metagenomics of the barley rhizosphere: the barley microbiome



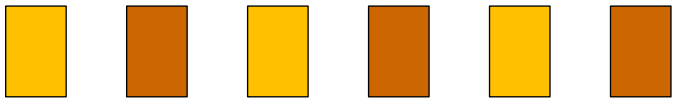
Golm soil #1

Golm soil #2



Rhizosphere DNA
2x soils; 3x reps

Pooling

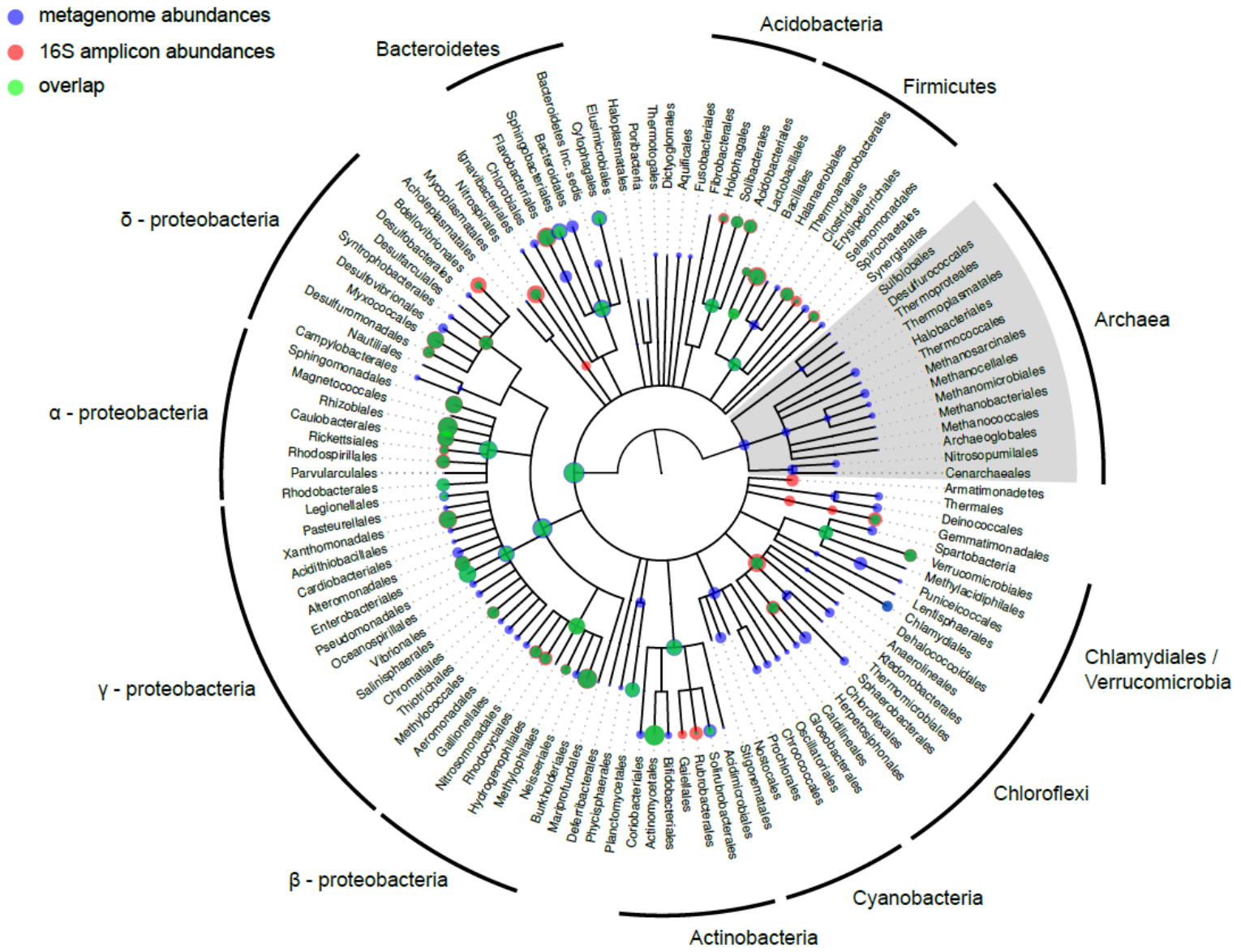


2x100bp, 25M PE reads x genotype X soil

QC, assembly, binning, annotation

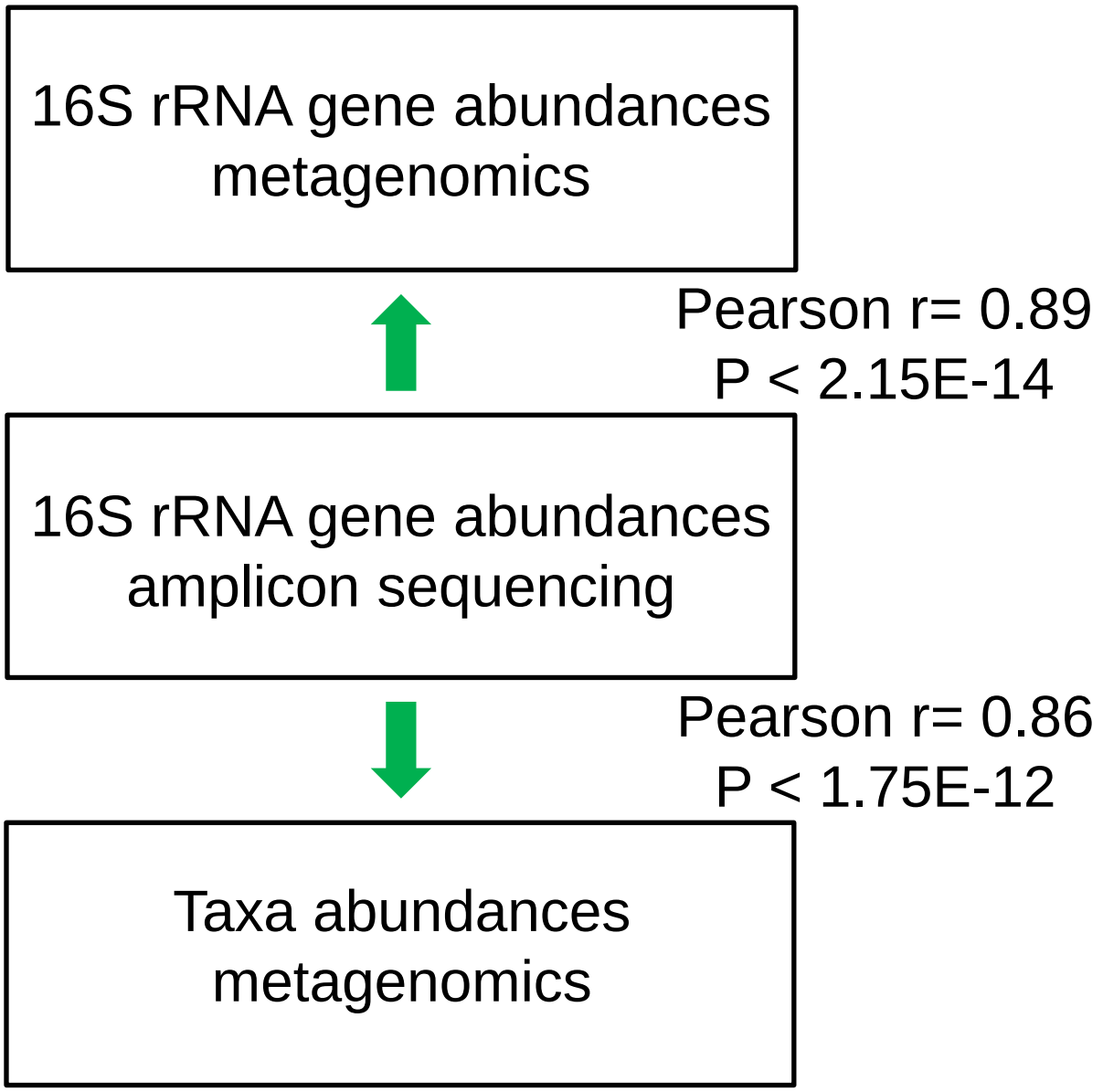
Microbiota taxa & functions

Bacteria dominate the annotated barley microbiome



Archaea 0.058% Eukaryotes 5.90% relative abundance

Amplicon *vs.* Metagenomics sequencing



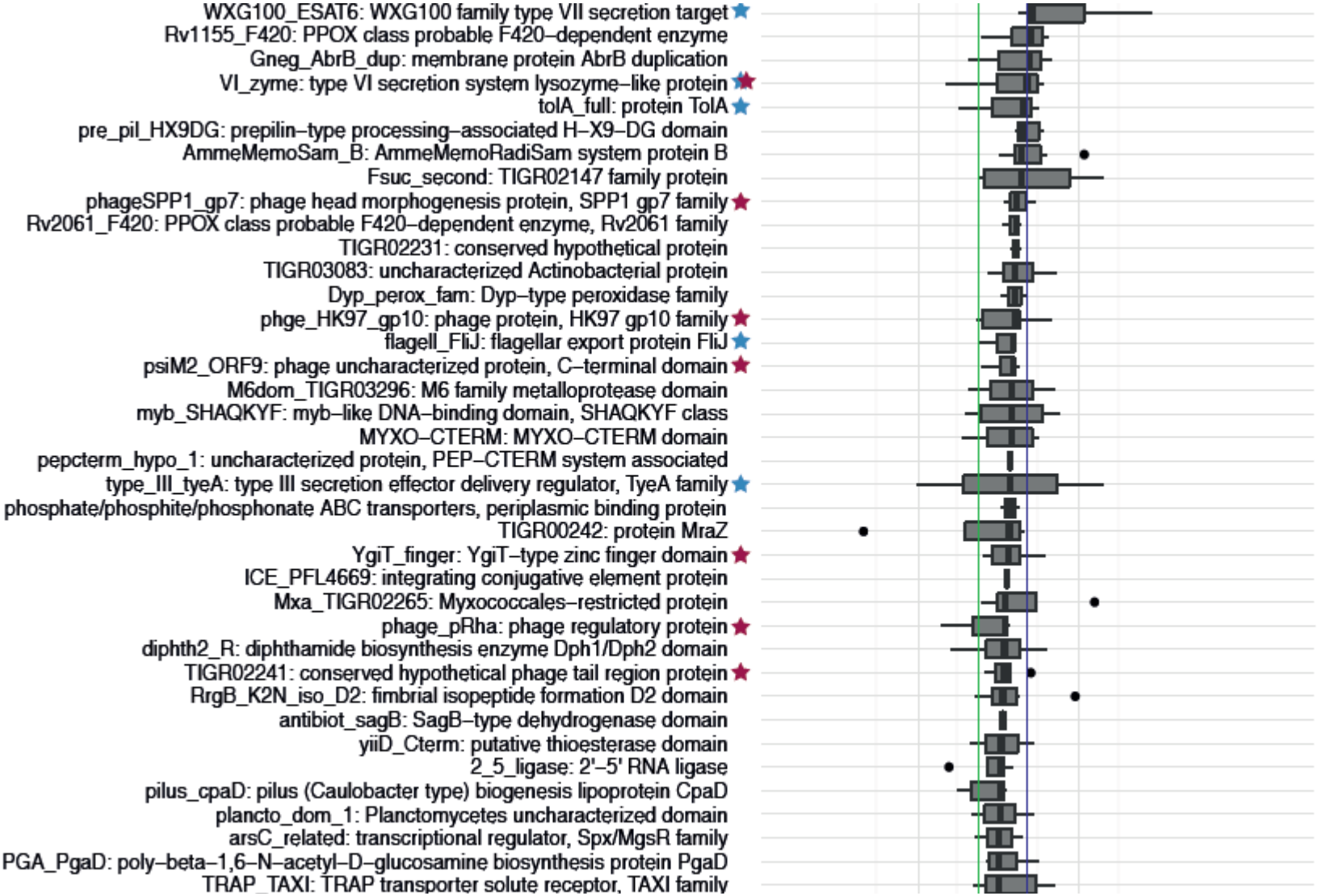
Linking structure and function

Table 1. Functions enriched in root and rhizosphere-associated bacterial taxa

Functional Category	P value*
Protein secretion system Type III	0.0013
Adhesion	0.0014
Regulation of virulence	0.0016
Siderophores	0.0016
Secretion	0.0053
Transposable elements	0.0138
Periplasmic Stress	0.0152
Sugar Phosphotransferase Systems	0.0209
Bacteriophage integration excision lysogeny	0.0300
Invasion and intracellular resistance	0.0300
Detoxification	0.0339
Protein secretion system Type VI	0.0339
Acid stress	0.0356

Bulgarelli *et al*. (2015), Cell Host Microbe 17:1

Positive selection in the barley rhizosphere



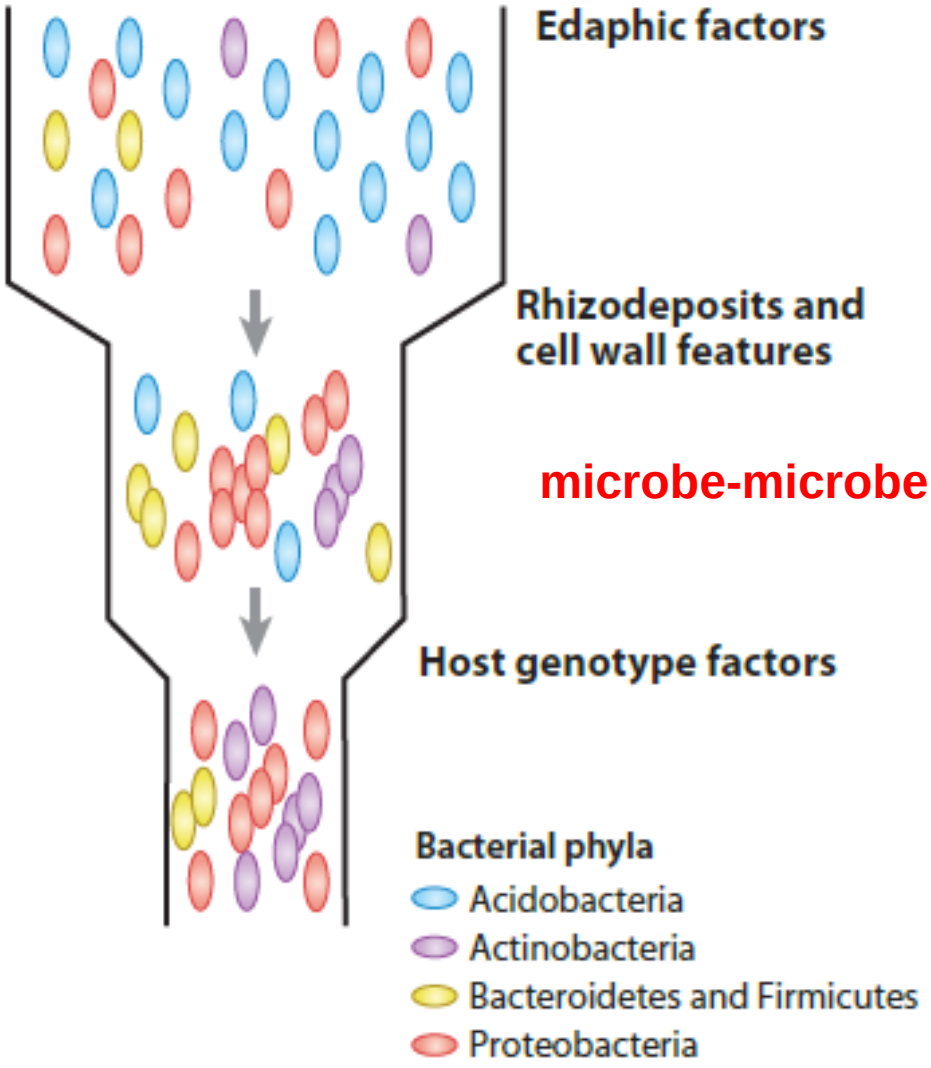
An evolutionary arms race in the barley rhizosphere?

A revised two-step process for the microbiome differentiation:

Soil

Rhizosphere

Root

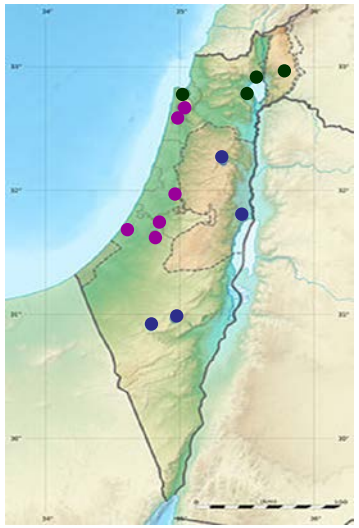


microbe-microbe interactions

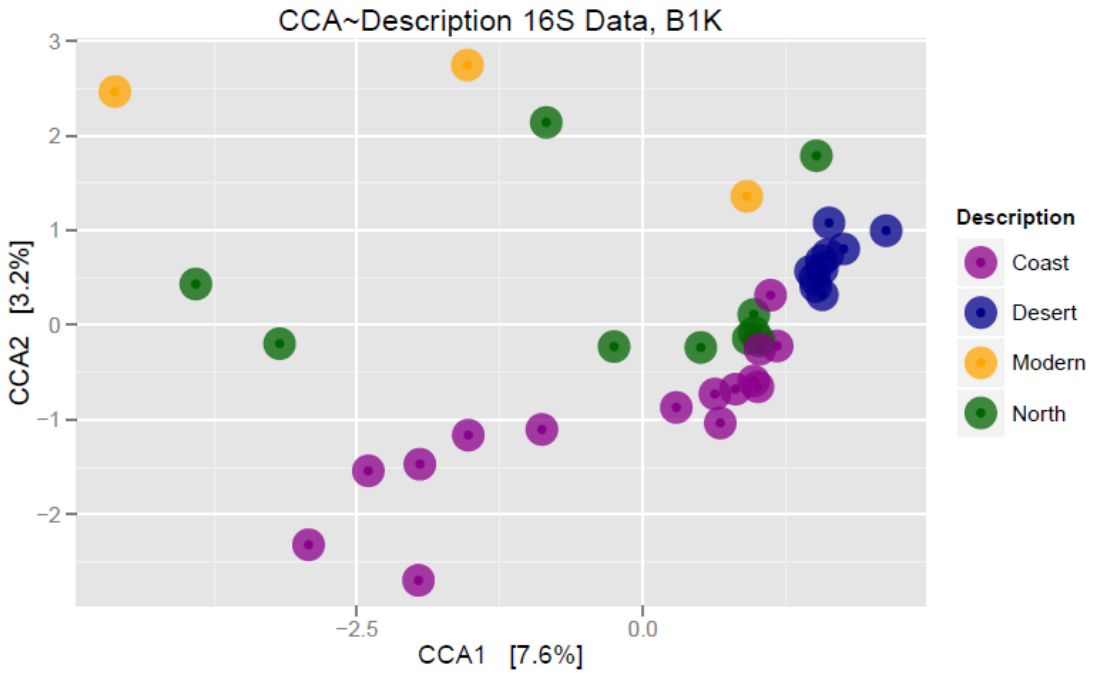
Bulgarelli *et al*. (2013) , Annu. Rev. Plant Bio. 64:807

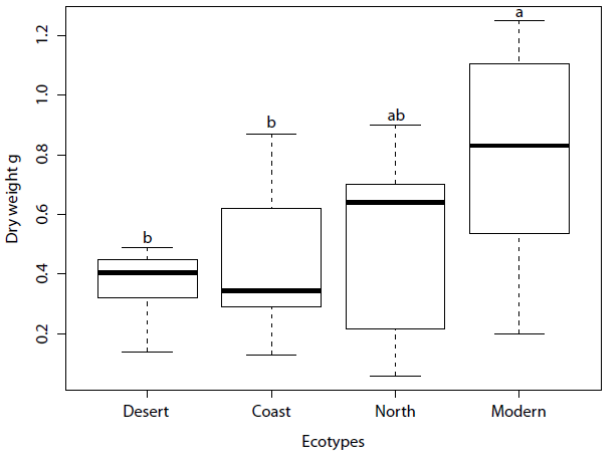
An on going co-evolutionary experiment

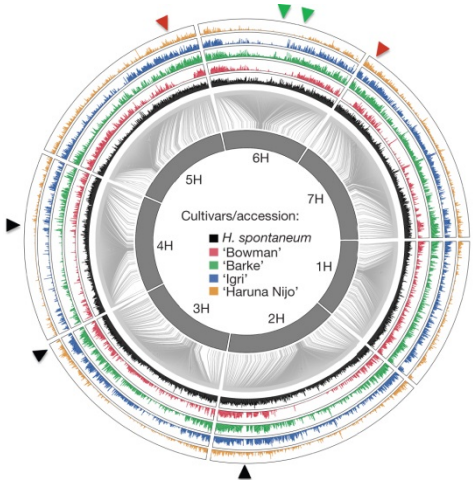
Wild barley ecotypes



- **North**
- **Coast**
- **Desert**

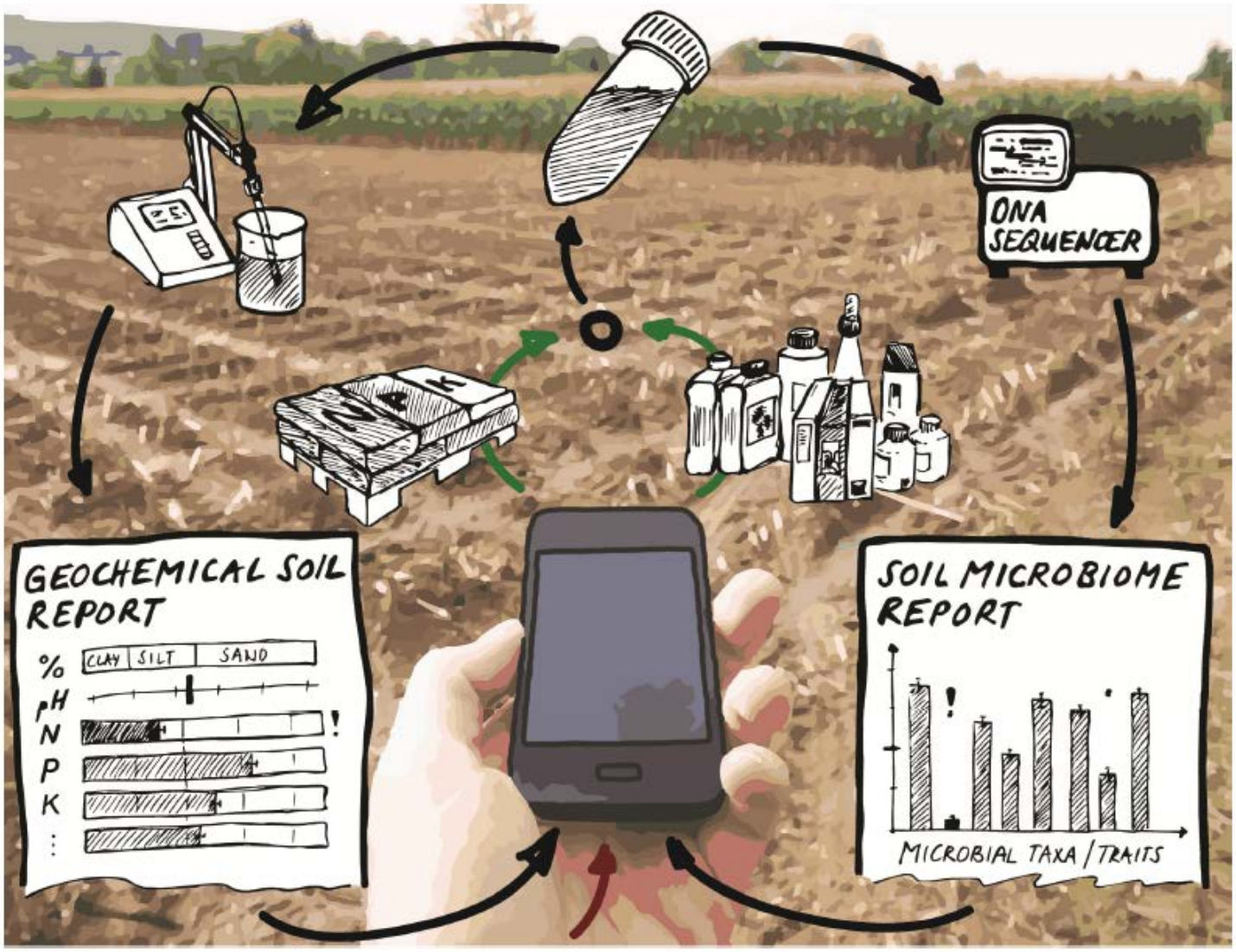






Rodrigo Alegria Terrazas

Next-generation agriculture



Schlaeppi and Bulgarelli (2014) , MPMI 28:212

Credits

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Rodrigo Alegria Terrazas
Looking for a PhD? Your name can be here...

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Isa Will
Maren Winnacker

Alice McHardy (HZI Braunschweig)
Philipp Münch
Johannes Dröge
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Eric Paterson (JHI Aberdeen)
Elizabeth Baggs (U Aberdeen)
Eyal Fridman (HU Jerusalem)

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